

**Table S3. Primers used in this study**

<b>Primer</b>	<b>Sequence (5'→3')<sup>a</sup></b>
psm $\alpha$ -FI	ctgcataacctccttatttctaac
psm $\alpha$ -RI	<b>AATCGTCAGTCAGTCACCATGGCA</b> taagattacctccttgcttatga
psm $\alpha$ -F2	<b>TGCCATGGTGA</b> CTGACTGACTGACGTAAtaatttaagcgaattgaactctaaa
psm $\alpha$ -R2	ggctaggacatgtatgtctta
psm $\beta$ -FI	<u>GGATCC</u> gtaatcacggaactctttgttt
psm $\beta$ -RI	<b>AATCGTCAGTCAGTCACCATGGCA</b> tgaaaacactccttaaaatttaatt
psm $\beta$ -F2	<b>TGCCATGGTGA</b> CTGACTGACTGACGTAAataataactaatattctttaaaataaactggg
psm $\beta$ -R2	<u>GGATCC</u> tgatacctgtttcttcagatataaatatc
GFPoptFR	<u>GAATTCAAGGAGGAAAAACATATGTCAA</u> AAGGAGAAGAATTAT
GFPoptRV	<u>GTCGAC</u> ttacttatataatcattcc

<sup>a</sup>The overlap in R1 and F2 primers used to merge flanking regions by PCR is shown in boldface. Restriction sites used for cloning are underlined. A ribosome-binding site is indicated in italics.